

Figure 1

fraction: M L 21 22 23 24 25 26 27 28 29 30 31 32

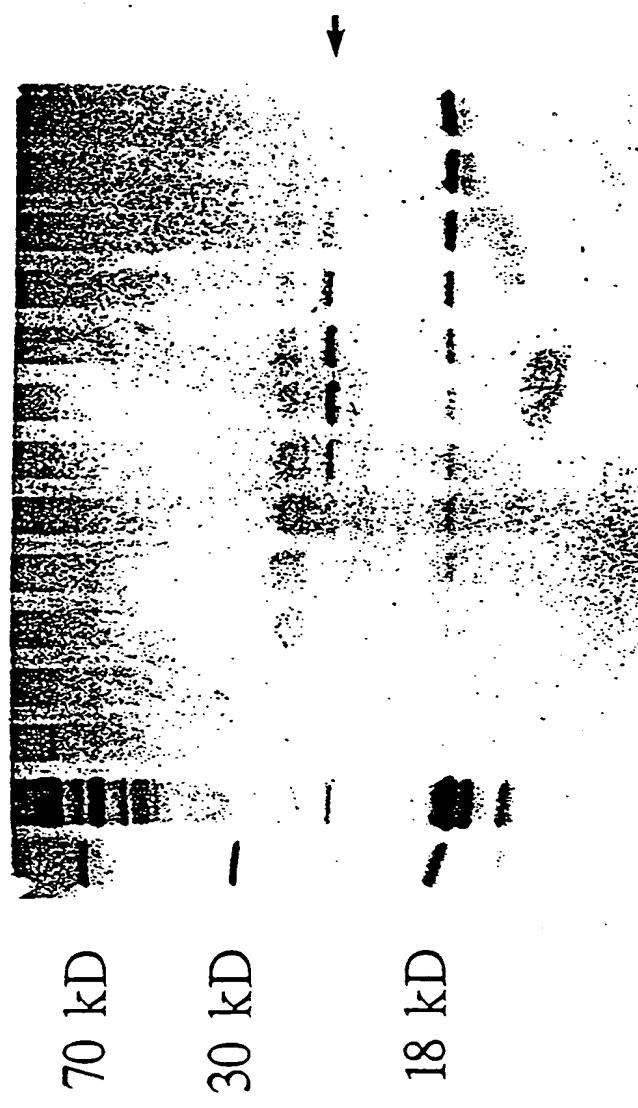


Figure 2a

SCG SURVIVAL

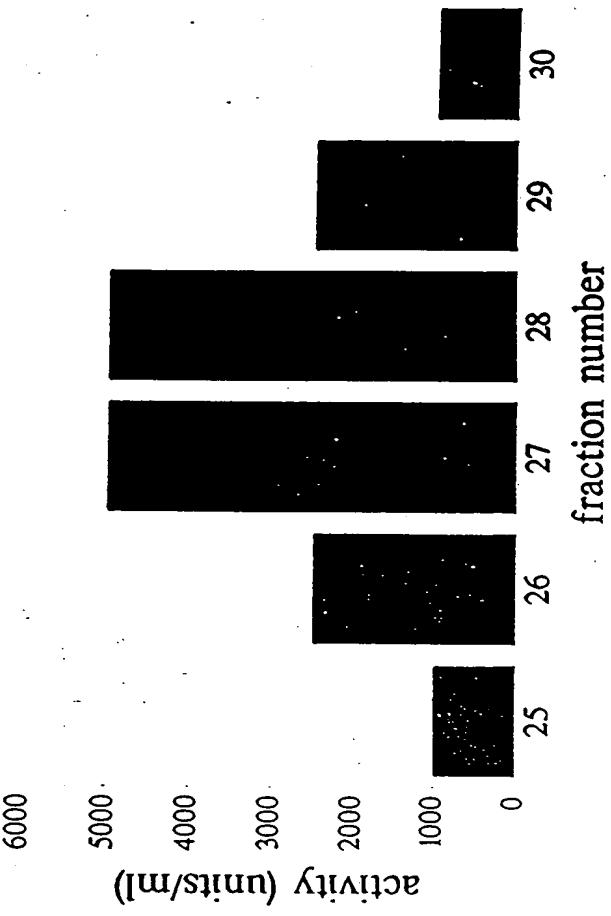


Figure 2b

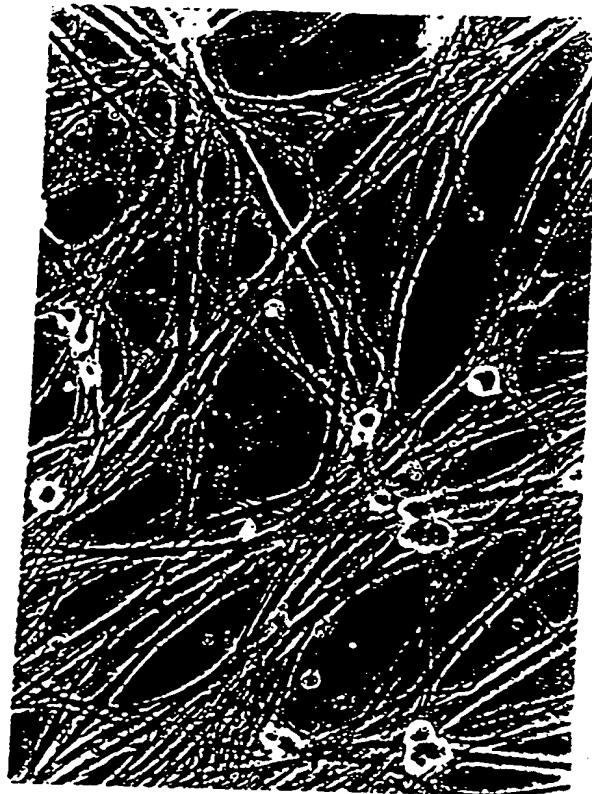


Figure 3a NGF

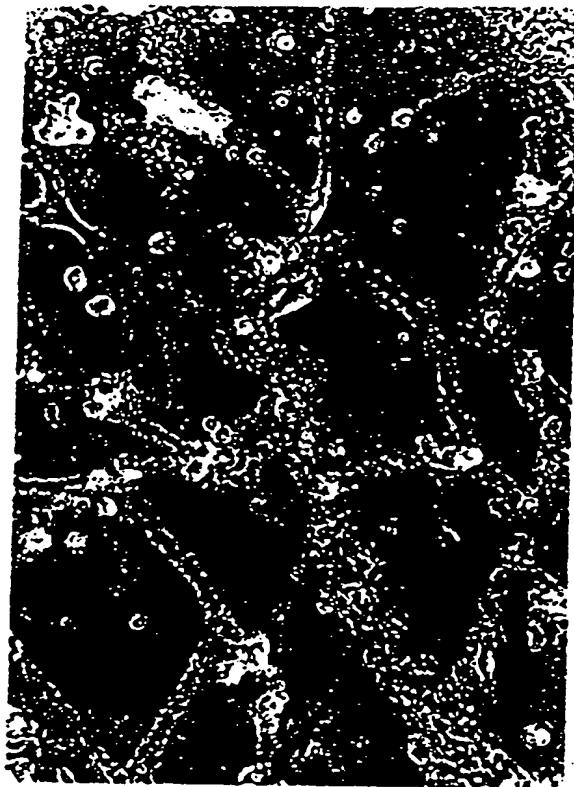


Figure 3b Anti-NGF

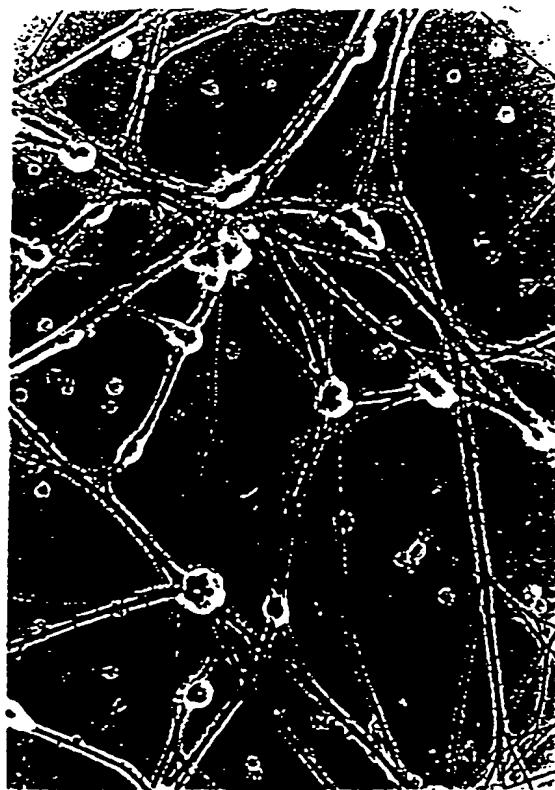


Figure 3c Anti-NGF
+
Neurturin

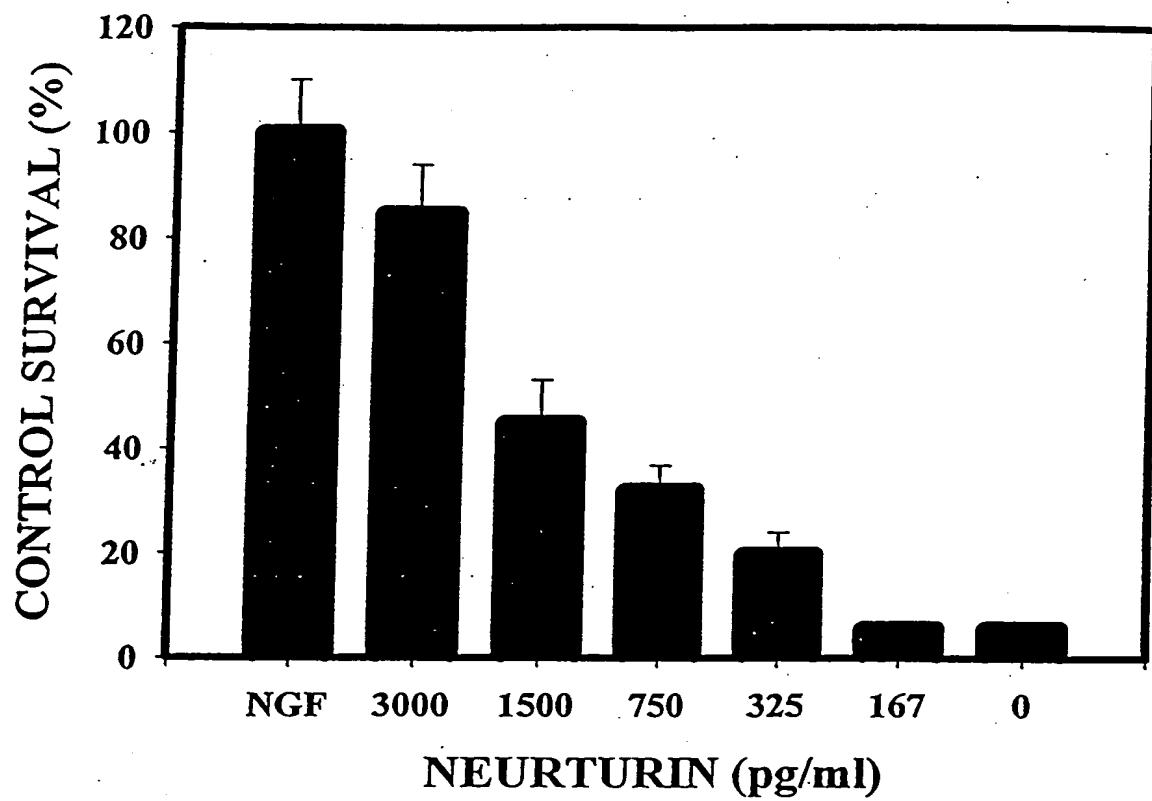
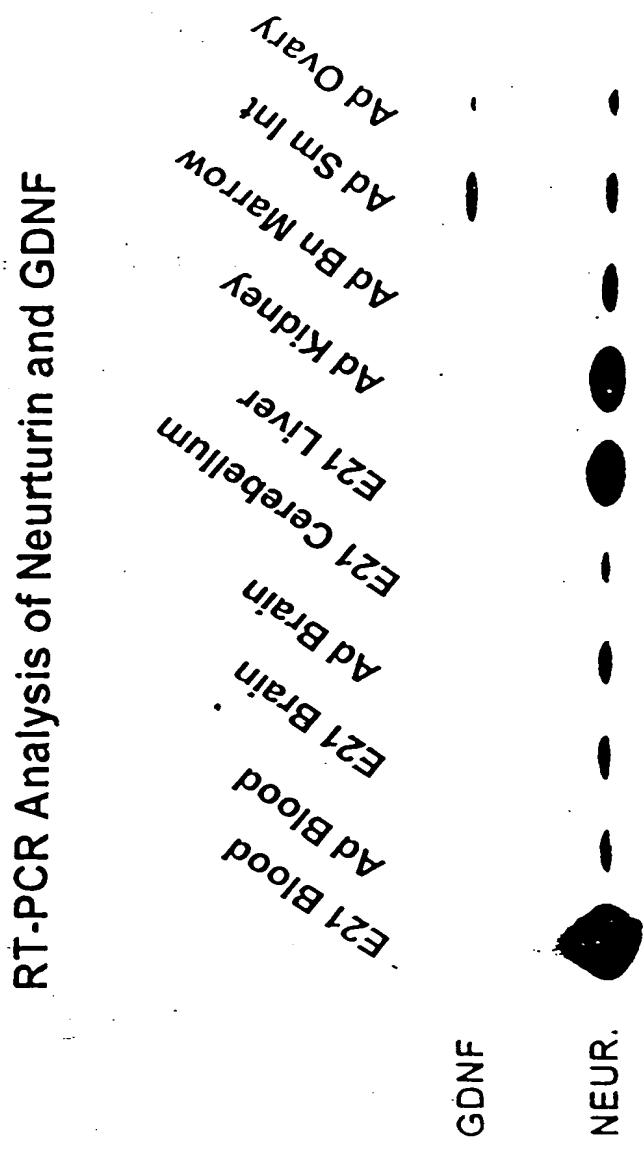


Figure 4

1	S P O K Q H A V L P R R E R N R Q A A A A N P E N S R G K G	hGONF
1	S P O K Q A A A L P R R E R N R Q A A A A S P E N S R G K G	mGONF
1	S P O K Q A A A L P R R E R N R Q A A A A S P E N S R G K G	rGONF
1	- - - - -	hNTN
1	- - - - -	mNTN
31	R R G Q R G K N R G C V L T A I H L N V T O L G L G Y E T K	hGONF
31	R R G Q R G K N R G C V L T A I H L N V T O L G L G Y E T K	mGONF
31	R R G Q R G K N R G C V L T A I H L N V T O L G L G Y E T K	rGONF
1	- - - A R L G A R P C G L R E L E V R V S E L G L G Y A S O	hNTN
1	- - - P G A R P C G L R E L E V R V S E L G L G Y T S D	mNTN
61	E E L I F R Y C S G S C D A A E T T Y D K I L K N L S R N R	hGONF
61	E E L I F R Y C S G S C E S A E T H Y D K I L K N L S R S R	mGONF
61	E E L I F R Y C S G S C E A A E T H Y D K I L K N L S R S R	rGONF
28	E T V L F R Y C A G A C E A A A R V Y D L G L R R L R Q R R	hNTN
26	E T V L F R Y C A G A C E A A I R I Y D L G L R R L R Q R R	mNTN
91	R L V S D K V - G Q A C C R P I A F D D O L S F L D D N L V	hGONF
91	R L T S D K V - G Q A C C R P V A F D D O D L S F L D D N L V	mGONF
91	R L T S D K V - G Q A C C R P V A F D D O D L S F L D D N L V	rGONF
58	R L R R R E R V R A Q P C C R P T A Y E D E V S F L D D O S L V	hNTN
56	R V R R E R A R A H P C C R P T A Y E D E V S F L D D V H S R	mNTN
120	Y H I L R K H S A K R C G C I .	hGONF
120	Y H I L R K H S A K R C G C I .	mGONF
120	Y H I L R K H S A K R C G C I .	rGONF
88	Y H T V H E L S A R E C A C C V .	hNTN
86	Y H T L Q E L S A R E C A C C V .	mNTN

Figure 5

Figure 6



ATGCAGCGCTGGAAGGCAGGCGGCTTGGCCTCAGTGCCTGCAGCTCCGTGCTGTCCATC 60
Met Gln Arg Trp Lys Ala Ala Leu Ala Ser Val Leu Cys Ser Ser Val Leu Ser Ile
TGGATGTGTCGAGAGGGCTGCTCTCAGCCACCGCCTGGACCTGCGCTGGTCCCTG 120
Trp Met Cys Arg Glu Gly Leu Leu Leu Ser His Arg Leu Gly Pro Ala Leu Val Pro Leu
CACCGCCTGCCTCGAACCTGGACGCCGGATTGCCCGCCTGGCCAGTACCGTGCACTC 180
His Arg Leu Pro Arg Thr Leu Asp Ala Arg Ile Ala Arg Leu Ala Gln Tyr Arg Ala Leu
CTGCAGGGGGCCCCGGATGCGATGGAGCTGCGCGAGCTGACGCCCTGGCTGGCGGCC 240
Leu Gln Gly Ala Pro Asp Ala Met Glu Leu Arg Glu Leu Thr Pro Trp Ala Gly Arg Pro
CCAGGTCCCGCGCCGTCGGCGGGCCCCGGCGCGCGCGCGTGCAGGGTTGGGGCG 300
Pro Gly Pro Arg Arg Arg Ala Gly Pro Arg Arg Arg Ala Arg Ala Arg Leu Gly Ala
CGGCCTTGCAGGGCTGCGCGAGCTGGAGGTGCGCGTGAGCGAGCTGGCCTGGCTACGCG 360
Arg Pro Cys Gly Leu Arg Glu Leu Glu Val Arg Val Ser Glu Leu Gly Leu Gly Tyr Ala
TCGGACGAGACGGTGCTGTTCCGCTACTGCGCAGGCCCTGCGAGGCTGCCCGCGTC 420
Ser Asp Glu Thr Val Leu Phe Arg Tyr Cys Ala Gly Ala Cys Glu Ala Ala Arg Val
TACGACCTCGGGCTGCGACGACTGCGCCAGCGGGCGCCTGCGGGAGCGGGTGC 480
Tyr Asp Leu Gly Leu Arg Arg Leu Arg Gln Arg Arg Leu Arg Arg Glu Arg Val Arg
GCGCAGCCCTGCTGCCCGACGGCTACGAGGACGAGGTGTCCTTCCTGGACGCGCAC 540
Ala Gln Pro Cys Cys Arg Pro Thr Ala Tyr Glu Asp Glu Val Ser Phe Leu Asp Ala His
AGCCGCTACCAACACGGTGCACGAGCTGCGCGCGAGTGCCTGCGTGTGA 594
Ser Arg Tyr His Thr Val His Glu Leu Ser Ala Arg Glu Cys Ala Cys Val

Figure 7

ATGAGGCCTGGAAGGCAGCGGCCCTGGTGTGCTCATCTGCAGCTCCCTGCTATCTGTC 60
Met Arg Arg Trp Lys Ala Ala Leu Val Ser Leu Ile Cys Ser Ser Leu Leu Ser Val
TGGATGTGCCAGGAGGGTCTGCTCTGGGCCACCGCCTGGACCCGCGCTTGCCCCGCTA 120
Trp Met Cys Gln Glu Gly Leu Leu Leu Gly His Arg Leu Gly Pro Ala Leu Ala Pro Leu
CGACGCCCTCCACGCACCCCTGGACGCCCGCATGCCCGCTGGCCAGTATCGCGCTCTG 180
Arg Arg Pro Pro Arg Thr Leu Asp Ala Arg Ile Ala Arg Leu Ala Gln Tyr Arg Ala Leu
CTCCAGGGCGCCCCCGACCGGGTGGAGCTTCGAGAACTTCTCCCTGGCTGCCGCATC 240
Leu Gln Gly Ala Pro Asp Ala Val Glu Leu Arg Glu Leu Ser Pro Trp Ala Ala Arg Ile
CCGGGACCGCGCCGTCGAGCGGGTCCCCGGCGTCGGCGGGCGCGGGGCTCGGCCT 300
Pro Gly Pro Arg Arg Arg Ala Gly Pro Arg Arg Arg Ala Arg Pro Gly Ala Arg Pro
TGTGGGCTGCGCGAGCTCGAGGTGCGCGTGAGCGAGCTGGCCTGGCTACACGTCGGAT 360
Cys Gly Leu Arg Glu Leu Glu Val Arg Val Ser Glu Leu Gly Leu Gly Tyr Thr Ser Asp
GAGACCGTGCTGTTCCGCTACTGCGCAGGCGCGTGCAGGGCGGCATCCGCATCTACGAC 420
Glu Thr Val Leu Phe Arg Tyr Cys Ala Gly Ala Cys Glu Ala Ala Ile Arg Ile Tyr Asp
CTGGGCCTTCGGCGCCCTGCGCCAGCGGAGGCAGTGCAGAGAGCGGGCGGGCGCAC 480
Leu Gly Leu Arg Arg Leu Arg Gln Arg Arg Arg Val Arg Arg Glu Arg Ala Arg Ala His
CCGTGTTGTCGCCGACGGCTATGAGGACGAGGTGTCCTTCTGGACGTGCACAGCCGC 540
Pro Cys Cys Arg Pro Thr Ala Tyr Glu Asp Glu Val Ser Phe Leu Asp Val His Ser Arg
TACCACACGCTGCAAGAGCTGCGCGGGAGTGCACGTGCGTGA 588
Tyr His Thr Leu Gln Glu Leu Ser Ala Arg Glu Cys Ala Cys Val

Figure 8

GGAGGGAGAGCGCGCGGTGGTTCGTCCGTGTGCCCGCGCCCCGGCGC	-301
TCCTCGCGTGGCCCCCGTCCCTGAGCGCGCTCCAGCCTCCCACGCGCGCC	-251
ACCCCGGGGTTCACTGAGCCCGGCGAGCCCCGGGAAGACAGAGAAAGAGA	-201
GGCCAGGGGGGGAAACCCATGGCCCGGCCGTGTCCCGCACCCGTGCGG	-151
TGGCCTCCTCCGGCACGGGTCCCCGGTCCGCTCCGGTCCCCGCGATCC	-101
GGATGGCGCACGCAGTGGCTGGGCCGGCGGGCTCGGTGGTCGGAGG	-51
AGTCACCACTGACCGGGTCATCTGGAGCCCGTGGCAGGCCGAGGCCAGG	-1
<u>ATGAGGCGCTGGAAGGCAGCGGCCCTGGTGTGCTCATCTGAGCTCCCT</u>	50
<u>GCTATCTGTCTGGATGTGCCAGGAGGGTCTGCTCTGGGCCACCGCTGG</u>	100
<u>GACCCGCGCTTGCCCCGCTACGACGCCCTCACGCACCCGGACGCCGC</u>	150
<u>ATCGCCCGCCTGGCCCAGTATCGCGCTCTGCTCCAGGGGCCCGACGC</u>	200
<u>GGTGGAGCTTCGAGAACTTCTCCCTGGCTGCCGCATCCGGGACCGC</u>	250
<u>GCCGTCGAGCGGGTCCCCGGCGTCGGCGGGCGCGGCCGGGCTCGGC</u>	300
<u>TGTGGCTGCGCGAGCTCGAGGTGCGCGTGGCGAGCTGGCCTGGCTA</u>	350
<u>CACGTCGGATGAGACCGTGCTGTTCCGCTACTGCGCAGGCGCGTGC</u>	400
<u>CGGCCATCCGCATCTACGACCTGGGCCTCGGCGCCTGCGCCAGCGGAGG</u>	450
<u>CGCGTGCAGAGAGAGCGGGCGCGGGCGCACCCGTGTGTCGCCCGACGG</u>	500
<u>CTATGAGGACGAGGTGTCCTTCCTGGACGTGCACAGCCGCTACCAACAC</u>	550
<u>TGCAAGAGCTGTCGGCGCGGGAGTGCGCGTGCCTGATGCTACCTCACG</u>	600
<u>CCCCCGACCTGCGAAAGGGCCCTCCCTGCCGACCCCTCGCTGAGAACTGA</u>	650
<u>CTTCACATAAAAGTGTGGGAACTCCC</u>	675

Figure 9

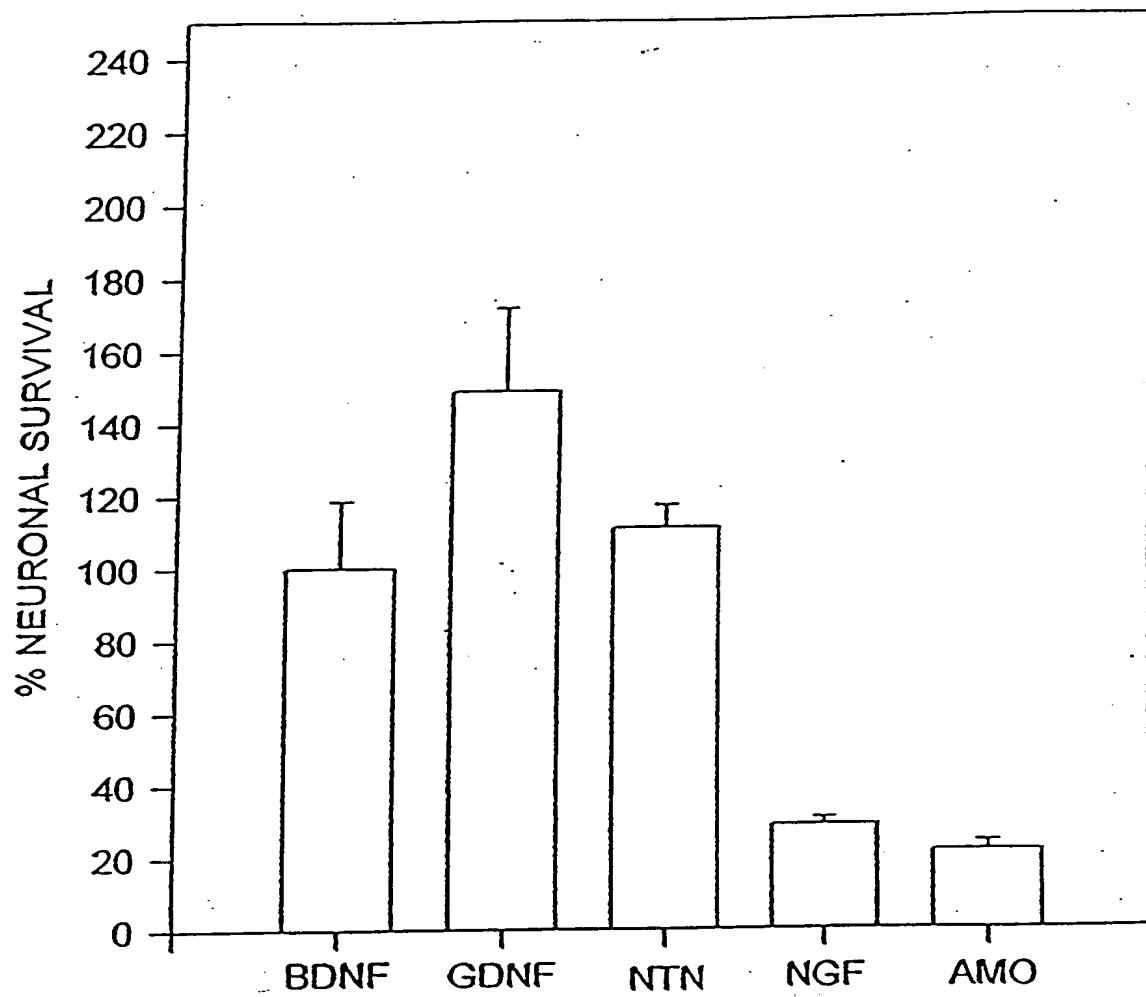


Figure 10

GAGGGACCTGGACGCCCATCAGGGTAAGAATTCTGGGGCCTCCGACTCCCCAATTC Glu Gly Pro Gly Arg Pro Ile Arg Val Arg Ile Pro Gly Gly Leu Pro Thr Pro Gln Phe	60 20
CTTCTCTCAAAGCCCTCACCTTGCTTACAATCCTACTCTACCTGCACTAGGTAAACAC Leu Leu Ser Lys Pro Ser Leu Cys Leu Thr Ile Leu Leu Tyr Leu Ala Leu Gly Asn Asn	120 40
CATGTCCGTCTTCCAAGAGCCTTGGCTGGTTCATGCCACTGTGGAGCCTGACCCCTACCA His Val Arg Leu Pro Arg Ala Leu Ala Gly Ser Cys Arg Leu Trp Ser Leu Thr Leu Pro	180 60
GTGGCTGAGCTGGCCTGGCTATGCCCTGGAGGAGAAGGTCACTTCCGATACTGTGCT Val Ala Glu Leu Gly Leu Gly Tyr Ala Ser Glu Glu Lys Val Ile Phe Arg Tyr Cys Ala	240 80
GGCAGCTGTCCCCAAGAGGCCGTACCCAGCACAGTCTGGTACTGGCCCGGCTCGAGGG Gly Ser Cys Pro Gln Glu Ala Arg Thr Gln His Ser Leu Val Leu Ala Arg Leu Arg Gly	300 100
CGGGGTGGAGCCCATGGCCGACCCCTGCCAGCCCACCGCTATGCTGATGTGACCTTC Arg Gly Arg Ala His Gly Arg Pro Cys Cys Gln Pro Thr Ser Tyr Ala Asp Val Thr Phe	360 120
CTTGATGATCAGCACCATGGCAGCAGCTGCCCTCAGCTCTCAGCTGCAGCTTGTGGCTGT Leu Asp Asp Gln His His Trp Gln Gln Leu Pro Gln Leu Ser Ala Ala Cys Gly Cys	420 140
GGTGGCTGAAGGAGGCCAGTCTGGTGTCTCAGAATCACAGCATGAGACAGGGCTGGCTT Gly Gly	480 142
TGAAAGGCTCAGGTGACATTACTAGAAATTGCATAGGTAAAGATAAGAAGGGAAAGGAC	540
CAGG	544

Figure 11

Figure 1.2

1	C	V	L	T	A	I	H	L	N	V	T	D	G	Y	E	T	K	E	L	F	R	C	S	E	-	S	A	E	T	W	D	K	I	L	K	N	L	S	R	S										
1	C	G	L	R	E	L	E	V	R	V	S	E	L	G	Y	T	S	D	E	T	V	F	R	C	G	A	C	E	A	A	I	R	I	-	Y	D	L	G	L	R	R	Q	R	N	N	P	S	P	S	P
1	C	R	L	W	S	L	T	P	V	A	E	L	G	Y	A	S	E	E	K	V	T	F	R	C	A	G	S	C	P	Q	E	A	R	T	Q	H	S	L	V	A	R	L	R	G	R	P				

50	R	R	L	T	S	D	K	V	-	G	Q	A	C	C	R	P	V	A	F	D	D	L	S	F	L	D	N	V	H	I	L	R	K	H	S	A	K	R	C	C	I		
50	R	R	V	R	R	A	H	P	C	P	T	A	Y	E	D	V	S	F	L	D	V	H	S	R	T	L	Q	E	S	A	R	E	C	A	V	;							
51	-	-	-	-	-	G	R	A	H	G	R	P	C	C	Q	P	J	S	Y	A	D	-	V	T	E	L	D	Q	H	H	Q	Q	L	P	Q	L	S	A	A	C	C	G	G

CCTCAGAGGAGAAGATTATCTTCCGATACTGTGCTGGCAGCTGTCCCCAAGAGGTCCGTACC	62
Ser Glu Glu Lys Ile Ile Phe Arg Tyr Cys Ala Gly Ser Cys Pro Gln Glu Val Arg Thr	20
CAGCACAGTCTGGTGCCTGGCCCGTCTTCGAGGGCAGGGTCGAGCTCATGGCAGACCTTGC	122
Gln His Ser Leu Val Leu Ala Arg Gly Gln Gly Arg Ala His Gly Arg Pro Cys	40
TGCCAGCCCACCAGCTATGCTGATGTGACCTTCCTTGATGACCACCACCATGGCAGCAG	182
Cys Gln Pro Thr Ser Tyr Ala Asp Val Thr Phe Leu Asp Asp His His His Trp Gln Gln	60
CTGCCTCAGCTCTCAGCCGCAGCTTGTGGCTGTGGTGGCTGAAGGCGGCCAGCCTGGTCT	242
Leu Pro Gln Leu Ser Ala Ala Cys Gly Cys Gly Gly	73
CTCAGAACATCACAGCAAGAGGGCAGCCTTGAAAGGCTCAGGTGACGTTATTAGAAACTTG	302
CATAGGAGAAGATTAAGAAGAGAAAGGGGACCTG	336

Figure 13

TGCCGGCTGTGGAGCCTGACCCCTACCAGTGGCTGAGCTTGGCCTGGCTATGCCTCAGAG	60
Cys Arg Leu Trp Ser Leu Thr Leu Pro Val Ala Glu Leu Gly Leu Gly Tyr Ala Ser Glu	20
GAGAAGATTATCTTCCGATACTGTGCTGGCAGCTGTCCCCAAGAGGTCCGTACCCAGCAC	120
Glu Lys Ile Ile Phe Arg Tyr Cys Ala Gly Ser Cys Pro Gln Glu Val Arg Thr Gln His	40
AGTCTGGTGCTGGCCCGTCTCGAGGGCAGGGTCGAGCTCATGGCAGACCTTGCTGCCAG	180
Ser Leu Val Leu Ala Arg Leu Arg Gly Gln Gly Arg Ala His Gly Arg Pro Cys Cys Gln	60
CCCACCAAGCTATGCTGATGTGACCTTCCTTGATGACCACCACATTGGCAGCAGCTGCCT	240
Pro Thr Ser Tyr Ala Asp Val Thr Phe Leu Asp Asp His His His Trp Gln Gln Leu Pro	80
CAGCTCTCAGCCGCAGCTTGTGGCTGTGGTGGCTGAAGGCGGCCAGCCTGGTCTCTCAGA	300
Gln Leu Ser Ala Ala Cys Gly Cys Gly Gly	91
ATCACAAAGCAAGAGGCAGCCTTGAAAGGCTCAGGTGACGTTATTAGAAACTTGCATAGG	360
AGAAGATTAAGAAGAGAAAGGGGACCTGATT	391

Figure 14

	10	20	30	40		
1	CVLTAIHLNV	TDLGLGYETKEELIFRYC	SGSCDAAETT-Y		GDNF(human)	
1	CVLTAIHLNV	TDLGLGYETKEELIFRYC	SGSCCEAAETH-Y		GDNF(rat)	
1	CVLTAIHLNV	TDLGLGYETKEELIFRYC	SGSCESAETH-Y		GDNF(mouse)	
1	CGLRELEV	RVSELGLGYASD	ETVLFRYCAGACEAAARV-Y		NTN(human)	
1	CGLRELEV	RVSELGLGYTSD	ETVLFRYCAGACEAAIRI-Y		NTN(mouse)	
1	CRLW	SLTLPV	VAELGLGYASEE	KIIFRYCAGSCPQEVR	TQH	PSP(rat)
1	CRLW	SLTLPV	VAELGLGYASEE	KVIFRYCAGSCPQEART	QH	PSP(mouse)
	50	60	70	80		
40	DKIL	IKNLSRNRRLV	SOKV-GQACC	RPPIAFD	DLSFLDDNL	GDNF(human)
40	DKIL	IKNLSRSRRLT	SOKV-GQACC	RPVAFD	DLSFLDDSL	GDNF(rat)
40	DKIL	IKNLSRSRRLT	SOKV-GQACC	RPVAFD	DLSFLDDNL	GDNF(mouse)
40	DLGL	RQRRRLRR	ERVRAQPCC	RPPTAYEDE	EVSFLOAHS	NTN(human)
40	DLGL	RQRRRVRR	RERARAHPC	RPPTAYEDE	EVSFLOVHS	NTN(mouse)
41	SLV	LARL	R-----	GQGRAHGRPCCQPTSYAD	-VTFLDDHH	PSP(rat)
41	SLV	LARL	R-----	GRGRAHGRPCCQPTSYAD	-VTFLDDQH	PSP(mouse)
	90					
79	VYHILRKH	SAKRCGC	C			GDNF(human)
79	VYHILRKH	SAKRCGC	C			GDNF(rat)
79	VYHILRKH	SAKRCGC	C			GDNF(mouse)
80	RYHTV	HELSARE	ECAC			NTN(human)
80	RYHTL	QELISARE	ECAC			NTN(mouse)
75	HWQQLPQL	SAAAAC	CGC			PSP(rat)
75	HWQQLPQL	SAAAAC	CGC			PSP(mouse)

Figure 15 A

1	A	L	A	G	S	C	R	L	W	S	L	T	L	P	V	A	E	L	G	L	G	Y	A	S	E	K	V	I	F		
1	A	L	P	G	L	C	R	L	W	S	L	T	L	P	V	A	E	L	G	L	G	Y	A	S	E	K	I	I	F		
1	A	L	S	G	P	C	Q	L	W	S	L	T	L	S	V	A	E	L	G	L	G	Y	A	S	E	K	V	I	F		
31	R	Y	C	A	G	S	C	P	Q	E	A	R	T	Q	H	S	L	V	L	A	R	L	R	G	R	A	H	G	60		
31	R	Y	C	A	G	S	C	P	Q	E	V	R	T	Q	H	S	L	V	L	A	R	L	R	G	Q	G	R	A	H	60	
31	R	Y	C	A	G	S	C	P	R	G	A	R	T	Q	H	G	L	A	L	Q	A	R	L	Q	G	Q	G	R	A	H	G
61	R	P	C	C	Q	P	T	S	Y	A	D	V	T	F	L	D	D	Q	H	H	W	Q	Q	L	P	Q	L	S	A	90	
61	R	P	C	C	Q	P	T	S	Y	A	D	V	T	F	L	D	D	H	H	H	W	Q	Q	L	P	Q	L	S	A	90	
61	G	P	C	C	R	P	T	R	Y	T	D	V	A	F	L	D	D	R	H	R	W	Q	R	L	P	Q	L	S	A		
91	A	A	A	A	C	C	C	C	G	G	G	G	G																		
91	A	A	A	A	C	C	C	C	G	G	G	G	G																		
91	A	A	A	A	C	C	C	C	G	G	G	G	G																		

Figure 15B

EQ	GROWTH FACTOR	SEQUENCE
0:		
50	TGF _B 1	CCVRQLY10FRKDLGKWIHEPKGYHANFCLGCPYIWSLDT-----QYSKVLALYQHNPGASSAA-PCCV--PQALEPLPIVYYVGRKPV--EQLSNMIVRSCKCS
51	TGF _B 2	CCRLRPLY10FRKDLGKWIHEPKGYHANFCAGACPYLWSSDT-----QHSRVLSLYNTINPEASAS-PCCV--SQDLEPLTILYYIGKTPK1--EQLSNMIVKSCKCS
52	TGF _B 3	CCVRPLY10FRQDLGKWIHEPKGYHANFCSGCPYLRSAQT-----THSTVLGLYNTLNPEASAS-PCCV--PQDLEPLTILYYIGRTPK--EQLSNMIVKSCKCS
53	INH _B A	CKKQFVFSFK-DIGWNDWIAPSGYHANYCEGCPSPHIAG-TSGSSLSFHFSTVINHYMRGHSPFANLKSCCV--PTKLRLPMSMLYYDQGQNI1-KDQNMIVEEGCS
54	INH _B B	CCRQQFF10FR-LIGWNDWIAPTYGGNNYCEGSCPAYLAG-VPGSASSSFHTAVVNYQYRMGLNP-GTVNNSCC1--PTKLSTMSMLYFDEENIV-KRDVPNMIVEEGCA
55	NODAL	CRRVKFOVDFN-LIGGSMWIYKQYNAVYCEGCPNPVGEEFHTP-----NHAYIQSSLKRYQPHR-YPSTCCA--PVKTKPLSMLYVDNGR--VLEHHKDMIVEEGCL
56	BMP2	CKRHPLYVDFS-DIGWNDWIAPPGYHAFYCHGCPFPPLADHLNST-----NHAIVQTLVNSVNS-K-IPKACCV--PTELSAISMLYLDENEKVVLK-NYQDMIVVEGGCR
57	BMP4	CRRHSLYVDFS-DIGWNDWIAPPGYQAFYCHGDCPFPPLADHLNST-----NHAIVQTLVNSVNS-S-IPKACCV--PTELSAISMLYLDYEOKVVLK-NYQEMIVVEGGCR
58	DPP	CRRHSLYVDFS-DIGWDDWIAPPGLYDAYYCHGKCPFPPLADHFNST-----NHAWQTLYNNMNPKG-VPKACCV--PTQLDSVAMLYLNQDSTVVLK-NYQEMTVVGGCR
59	BMP5	CKKHLYVSFR-DLGQDWWIAPEGYAAFYCDGECSPFLNAHMNAT-----NHAIVQTLVHLMFPDH-VPKPCCA--PTKLNAISVLYFDDSSNVILK-KYRNMIVVRCGCH
60	BMP6	CRKHLYVSFR-DLGWQDWWIAPKGYAANYCDGECSPFLNAHMNAT-----NHAIVQTLVHLMNPEY-VPKPCCA--PTKLNAISVLYFDDDSNVILK-KYRNMIVVRCGCH
61	BMP7	CKKHLYVSFR-DLGWQDWWIAPEGYAAFYCEGECAPLNSYMMAT-----NHAIVQTLVHFTNPET-VPKPCCA--PTQLNNAISVLYFDDSSNVILK-KYRNMIVVRCGCH
62	BMP8	CRRHLYVSFR-DLGWLDWWIAPQGYSAYYCEGECSPFLDSCMNAAT-----NHAILQSLVHLMKPNA-VPKACCA--PTKLTSATSVLYYDSSNNVILR-KHNMIVVACGCH
63	60A	CQMTQY1DFK-DLGWHDWIAPEGYGAFCSGECNFPLNAHMNAT-----NHAIVQTLVHILLEPKK-VPKPCCA--PTRLGALPVLYHLDENVNVLK-KYRNMIVVSCGCH
64	BMP3	CARRYLKVOFA-DIGWSEWIIISPKSFDAYYCSGACQFMPKSLKPS-----NHAITQSIIVRAYGVPGIPEPCCV--PEKMSSLISLFFDENKNVVLK-V-YPNMTVSESCACR
65	VG1	CKKRHLYVEFK-DVGWQNWWIAPQGYMANCYGECPYPLTEIILNGS-----NHAILQTLVHSIEPD-IPLPPCCV--PTKMSPIISMLFYDNNDNVVLR-HYENMADECGGCR
66	GDF1	CRARRLYVSFR-EVGWHRWVIAPRGFLANYCQGQCALPVALSGSGGPPALNHAVRLALMHAAPGA--ADLPPCCV--PARLSPISVLFFDNSDNVVLR-QYEDMVVDEGGCR
67	GDF3	CHR10LFINFO-DLGWHWKWIAPKGFMANYCHGECPFSMTTYLNS-----NAYFMQALMHIMADP-K-VPKAVCV--PTKLSPISMLYQDSOKAVILR-HYEDMVVDEGGCG
68	DORSLN	CRTTSLHVNFK-EIGWDSWIAPKDYAEFECKGGCFPLTDNVTPT-----KHAIVQTLVHLONPKK-ASKACCV--PTKLDAISILYKDDAGVPTL1NYEGMKVAECGCR
69	INHA	CHRVALNISF-QELGWERWIVYPPSF1FHYCHGGCGLHIPPNLSLPVPGAPPTPAQPSLL-----PGAQPCCAAALPGTMRLHVRRTSDGGYSFKYETVPNLLTOHCACI
70	MIS	CALRELSVOLRAERS-----VL1PETYQANNQGACGMQSDR--NPRYGNHVULLKMQARGATLARPPCCV--PTAYT-GKLISISSEERISAHVPMVATEGGCR
71	GDF9	CELHDFSLFS-QLKWDNWIVAPHSYNPSYCKGDCPSAVSHRGSPV--HTMVQNMIE-KLDPSVSPSPSCV--PGKYSPLSVLTIEPDGSTAYK-EYEDMMATSCTCR
72	GDNF	CVLTAIHLNVT-DLGGLG--YETKEELIFRYCGSGSCD-AAETTYDKILKLNLSRN-----RRLYSDKV-GOACCRPIAFD-DDLSFL-----DDNLVYHILRKHSAKRCGC1
73	NTN	CGLRELEVRVS-ELGLG--YASDETVLFRYCAVACE-AAARVYDGLRRLRQF-----DAHSRYHTVHELSARECACV

FIGURE 16

1 ATGGCTGCAG GAAGACTTCG GATCCTGTGT CTGCTGCTCC TGTCCCTGCA CCCGAGCCTC
 TACCGACGTC CTTCTGAAGC CTAGGACACA GACGACGAGG ACAGGAACGT GGGCTCGGAG
 61 GGCTGGGTCC TTGATCTTCA AGAGGCTTCT GTGGCAGATA AGCTCTCATT TGGGAAGATG
 CCGACCCAGG AACTAGAAGT TCTCCGAAGA CACCGTCTAT TCGAGAGTAA ACCCTTCTAC
 ↓
 121 GCAGAGACTA GAGGGACCTG GACGCCCAT CAGGGTAAGA ATTCCTGGGG GCCTCCGAC
 CGTCTCTGAT CTCCCTGGAC CTGCGGGGT A GTCCCATTCT TAAGGACCCC CGGAGGGCTG
 ↓
 181 TCCCCAATT C CTTCTCTCAA AGCCCTCACT TTGCCTTACA ATCCTACTCT ACCTTGCAC
 AGGGGTTAAG GAAGAGAGTT TCGGGAGTGA AACGGAATGT TAGGATGAGA TGGAACGTGA
 ↓
 241 AGGTAAACAAAC CATGTCCGTC TTCCAAGAGGC CTTGGCTGGT TCATGCCGAC TGTGGAGCCT
 TCCATTGTTG GTACAGGCAG AAGGTTCTCG GAACCGACCA AGTACGGCTG ACACCTCGGA
 301 GACCCTACCA GTGGCTGAGC TGGGCCTGGG CTATGCCCG GAGGAGAAGG TCATCTCCG
 CTGGGATGGT CACCGACTCG ACCCGGACCC GATAACGGAGC CTCCTCTTCC AGTAGAAGGC
 361 ATACTGTGCT GGCAGCTGTC CCCAAGAGGC CCGTACCCAG CACAGTCTGG TACTGGCCCG
 TATGACACGA CCGTCGACAG GGGTTCTCCG GGCATGGTC GTGTCAGACC ATGACCGGGC
 421 GCTTCGAGGG CGGGGTCGAG CCCATGGCCG ACCCTGCTGC CAGCCCACCA GCTATGCTGA
 CGAAGCTCCC GCCCCAGCTC GGGTACCGGC TGGGACGACG GTCGGGTGGT CGATACGACT
 481 TGTGACCTTC CTTGATGATC AGCACCATTG GCAGCAGCTG CCTCAGCTCT CAGCTGCAGC
 ACACTGGAAG GAACTACTAG TCGTGGTAAC CGTCGTCGAC GGAGTCGAGA GTCGACGTCG
 541 TTGTGGCTGT GGTGGCTGAA GGAGGCCAGT CTGGTGTCTC AGAATCACAA GCATGAGACA
 AACACCGACA CCACCGACTT CCTCCGGTCA GACCACAGAG TCTTAGTGTGTT CGTACTCTGT
 601 GGCTGGGCTT TGAAAGGCTC AGGTGACATT ACTAGAAATT TGCATAGGTA AAGATAAGAA
 CCGACCCGAA ACTTCCGAG TCCACTGTAA TGATCTTAA ACGTATCCAT TTCTATTCTT
 661 GGGAAAGGAC CAGGGGTTTT TTGTTCTTT CTTTGCTTGC TTGTTAGTTT TTTTTTTTT
 CCCTTCCTG GTCCCCAAAA AACAAAGAAA GAAACGAACG AACAAATCAA AAAA
 721 TTT
 AAA

Figure 17A

1 ATGGCTGCAG GAAGACTTCG GATCCTGTGT CTGCTGCTCC TGTCCTTGCA CCCGAGCCTC
 TACCGACGTC CTTCTGAAGC CTAGGACACA GACGACGAGG ACAGGAACGT GGGCTCGGAG
 1 M A A G R L R I L C L L L S L H P S L
 61 GGCTGGGTCC TTGATCTTCA AGAGGGCTTCT GTGGCAGATA AGCTCTCATT TGGGAAGATG
 CCGACCCAGG AACTAGAAGT TCTCCGAAGA CACCGTCTAT TCGAGAGTAA ACCCTTCTAC
 21 G W V /L D L Q E A S V A D K L S F G K M
 ↓
 121 GCAGAGACTA GAGGGACCTG GACGCCCAT CAGGGTAACA ACCATGTCCG TCTTCCAAGA
 CGTCTCTGAT CTCCCTGGAC CTGCGGGGT A GTCCCATTGT TGGTACAGGC AGAAGGTTCT
 41 A E T R G T W T P H Q G N N H V R L P R
 181 GCCTTGGCTG GTTCATGCCG ACTGTGGAGC CTGACCCCTAC CAGTGGCTGA GCTGGGCTG
 CGGAACCGAC CAAGTACGGC TGACACCTCG GACTGGGATG GTCAACCGACT CGACCCGGAC
 61 A L A G S C R L W S L T L P V A E L G L
 241 GGCTATGCCCT CGGAGGAGAA GGTCACTTTC CGATACTGTG CTGGCAGCTG TCCCCAAGAG
 CCGATACGGA GCCTCCTCTT CCAGTAGAAG GCTATGACAC GACCGTCGAC AGGGGTTCTC
 81 G Y A S E E K V I F R Y C A G S C P Q E
 301 GCCCGTACCC AGCACAGTCT GGTACTGGCC CGGCTTCGAG GGCAGGGTCG AGCCCATGGC
 CGGGCATGGG TCGTGTCAAGA CCATGACCGG GCCGAAGCTC CCGCCCCAGC TCGGGTACCG
 101 A R T Q H S L V L A R L R G R G R A H G
 361 CGACCCCTGCT GCCAGCCCAC CAGCTATGCT GATGTGACCT TCCTTGATGA TCAGCACCCT
 GCTGGGACGA CGTCGGGTG GTCGATACGA CTACACTGGA AGGAACTACT AGTCGTGGTA
 121 R P C C Q P T S Y A D V T F L D D Q H H
 421 TGGCAGCAGC TGCTCAGCT CTCAGCTGCA GCTTGTGGCT GTGGTGGCTG A
 ACCGTCGTCG ACGGAGTCGA GAGTCGACGT CGAACACCGA CACCAACCGAC T
 141 W Q Q L P Q L S A A A C G C G G

Figure 17B

1 ATGGCTGCAG GAAGACTTCG GATCTTGT TT CTGCTGCTCC TGTCCCTGCA CCTGGGCCTT
TACCGACGTC CTTCTGAAGC CTAGAACAAA GACGACGAGG ACAGGAACGT GGACCCGGAA
61 GGCTGGGTCC TTGATCTTCA AGAGGCTCCT GC GG CAGATG AGCTCTCATC TGGGAAAATG
CCGACCCAGG AACTAGAAGT TCTCCGAGGA CGCCGTCTAC TCGAGAGTAG ACCCTTTAC
121 GCAGAGACTG GAAGGACCTG GAAGCCCCAT CAGGGTAAGA ATTCTTGGGG GCCTCCTAAC
CGTCTCTGAC CTTCCGGAC CTTCGGGTA GTCCCATTCT TAAGAACCCC CGGAGGATTG
181 TCTACAGTTC TTCCCTCTCAA AGCCCTCACT TTGCCTCACA ATCCTATTCT ACCTTGCAC
AGATGTCAAG AAGGAGAGTT TCGGGAGTGA AACGGAGTGT TAGGATAAGA TGGAACGTGA
241 AGGTAAACAAC AATGTCCGCC TTCCAAGAGC CTTACCTGGT TTGTGCCGGC TGTGGAGCCT
TCCATTGTTG TTACAGGCCG AAGTTCTCG GAATGGACCA AACACGGCCG ACACCTCGGA
301 GACCCTACCA GTGGCTGAGC TTGGCCTGGG CTATGCCTCA GAGGAGAAGA TTATCTTCCG
CTGGGATGGT CACCGACTCG AACCGGACCC GATA CGGAGT CTCCTCTTCT AATAGAACGC
361 ATACTGTGCT GGCAGCTGTC CCCAAGAGGT CCGTACCCAG CACAGTCTGG TGCTGGCCCG
TATGACACGA CCGTCGACAG GGGTTCTCCA GGCATGGTC GTGTCAGACC ACGACCGGGC
421 TCTTCGAGGG CAGGGTCGAG CTCATGGCAG ACCTTGCTGC CAGCCCACCA GCTATGCTGA
AGAAGCTCCC GTCCCAGCTC GAGTACCGTC TGGAACGACG GTCGGGTGGT CGATACGACT
481 TGTGACCTTC CTTGATGACC ACCACCATTG GCAGCAGCTG CCTCAGCTCT CAGCCGCAGC
ACACTGGAAG GAACTACTGG TGGTGGTAAC CGTCGTCGAC GGAGTCGAGA GTCGGCGTCG
541 TTGTGGCTGT GGTGGCTGA
AACACCGACA CCACCGACT

Figure 18A

1 ATGGCTGCAG GAAGACTTCG GATCTTGTCTT CTGCTGCTCC TGTCCCTGCA CCTGGGCCTT
 TACCGACGTC CTTCTGAAGC CTAGAACAAA GACGACGAGG ACAGGAACGT GGACCCGGAA
 1 M A A G R L R I L F L L L L S L H L G L

 61 GGCTGGGTCC TTGATCTTCA AGAGGCTCCT GCAGGAGATG AGCTCTCATC TGGGAAAATG
 CCGACCCAGG AACTAGAAGT TCTCCGAGGA CGCCGTCTAC TCGAGAGTAG ACCCTTTAC
 21 G W V L D L Q E A P A A D E L S S G K M

 121 GCAGAGACTG GAAGGACCTG GAAGCCCCAT CAGGGTAACA ACAATGTCCG CCTTCCAAGA
 CGTCTCTGAC CTTCCCTGGAC CTTCGGGTA GTCCCATTGT TGTACAGGC GGAAGGTTCT
 41 A E T G R T W K P H Q G N N N V R L P R

 181 GCCTTACCTG GTTTGTGCCG GCTGTGGAGC CTGACCCCTAC CAGTGGCTGA GCTTGGCCTG
 CGGAATGGAC CAAACACGGC CGACACCTCG GACTGGGATG GTCAACCGACT CGAACCGGGAC
 61 A L P G L C R L W S L T L P V A E L G L

 241 GGCTATGCCT CAGAGGAGAA GATTATCTTC CGATACTGTG CTGGCAGCTG TCCCCAAGAG
 CCGATACGGA GTCTCCTCTT CTAATAGAAG GCTATGACAC GACCGTCGAC AGGGGTTCTC
 81 G Y A S E E K I I F R Y C A G S C P Q E

 301 GTCCGTACCC AGCACAGTCT GGTGCTGGCC CGTCTTCGAG GGCAAGGGTCG AGCTCATGGC
 CAGGCATGGG TCGTGTCAAGA CCACGACCGG GCAGAACGTC CCGTCCCAGC TCGAGTACCG
 101 V R T Q H S L V L A R L R G Q G R A H G

 361 AGACCTTGCT GCCAGCCCCAC CAGCTATGCT GATGTGACCT TCCTTGATGA CCACCAACCAT
 TCTGGAACGA CGGTCGGGTG GTCGATACGA CTACACTGGA AGGAACACT GGTGGTGGTA
 121 R P C C Q P T S Y A D V T F L D D H H H

 421 TGGCAGCAGC TGCCTCAGCT CTCAGCCGCA GCTTGTGGCT GTGGTGGCTG A
 ACCGTGTCG ACGGAGTCGA GAGTCGGCGT CGAACACCGA CACCACCGAC T
 141 W Q Q L P Q L S A A A C G C G G

Figure 18B

Figure 19

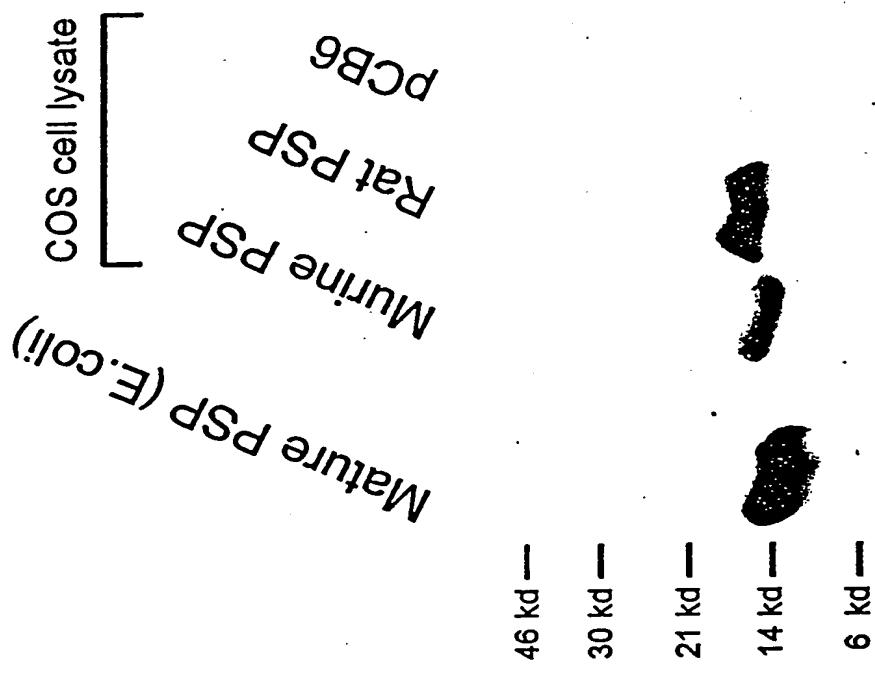


FIGURE 20A

PSP/NTN (SEQ ID NO:137)

ALAGSCRLWSLTLPVAELGLGYASEEKVIFRYCAGSCPQEARTQHSLVLA	50
↓	
RLRGRGRAHGRPCCRPTAYEDEVSFLDVHSRYHTLQELSARECACV	96

FIGURE 20B

NTN/PSP (SEQ ID NO:142)

PGARPCGLRELEVRSSELGLGYTSDETVLFRYCAGACEAAIRIYDLGLRR	50
↓	
LRQRRRVRRERARAHPCQOPTSYADVTFLDDQHHWQQLPQLSAAACGCGG	100

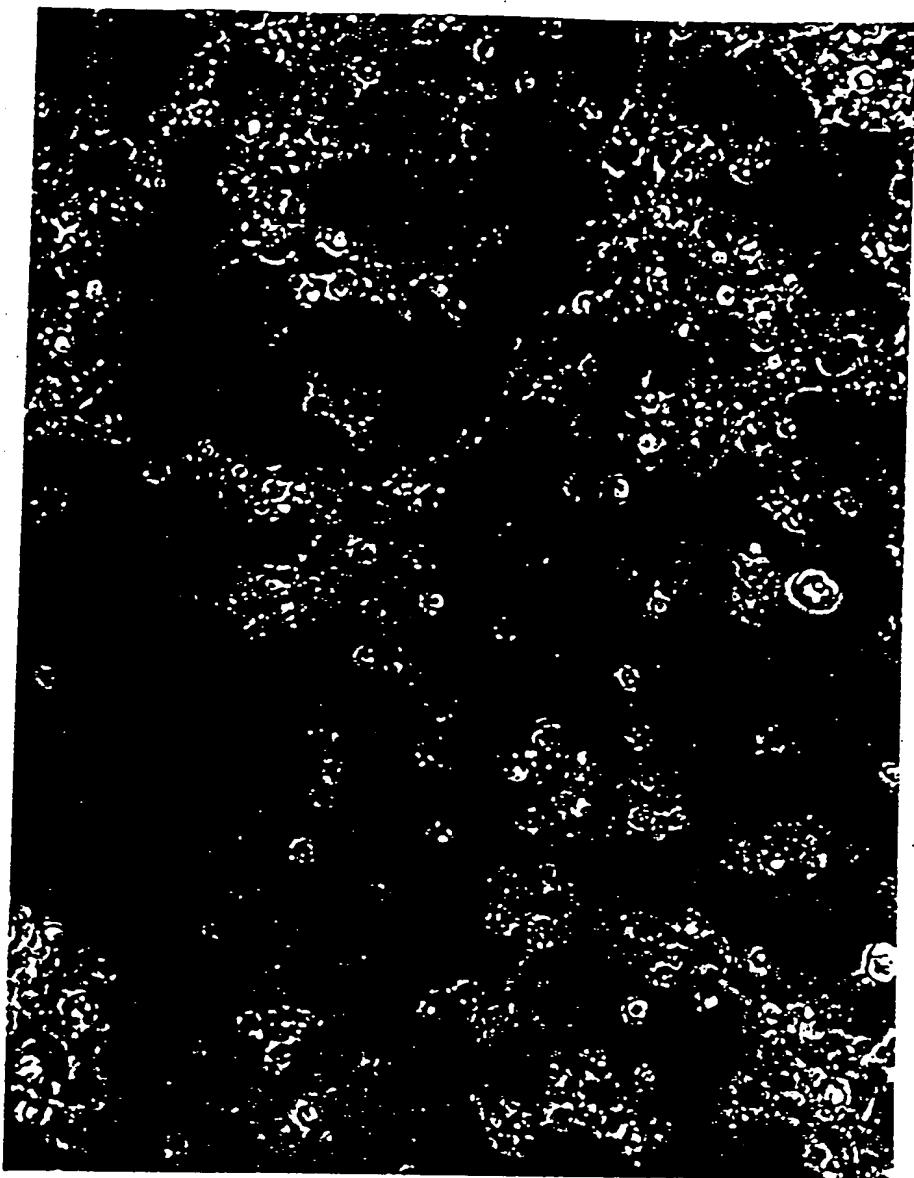


Figure 21a



Figure 21b

TOH labeled cells in E14 mesencephalic cultures

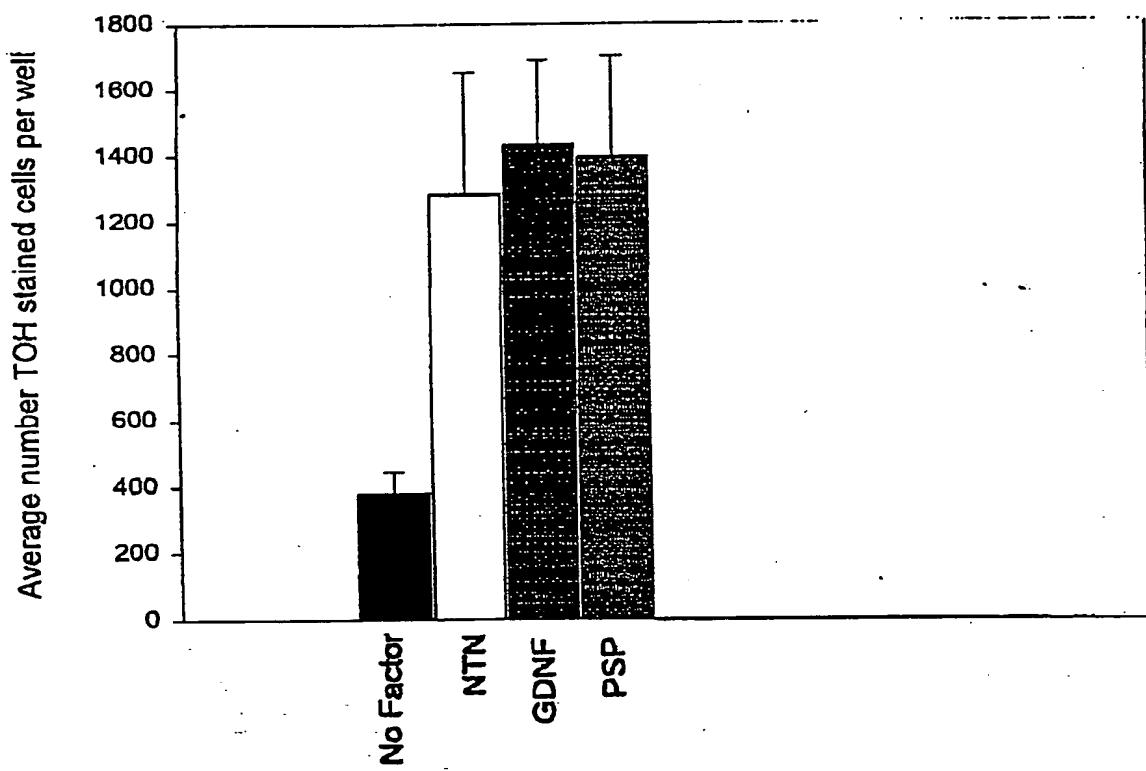


Figure 22

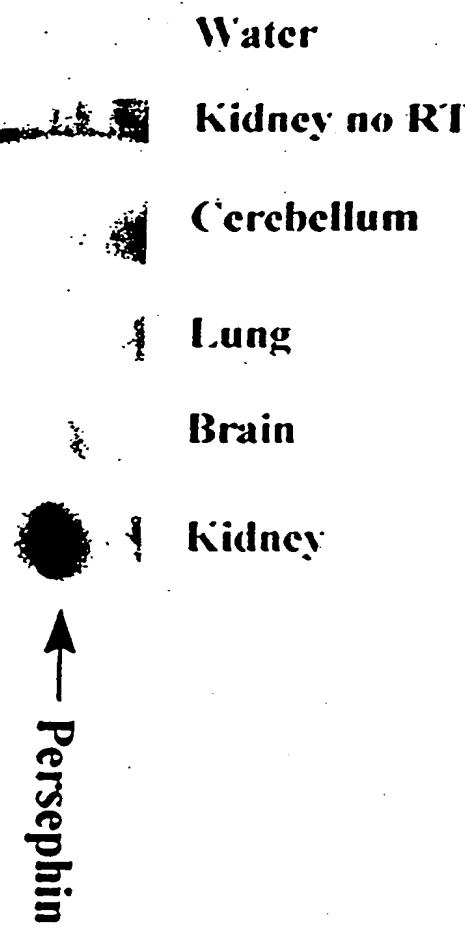


Figure 23

1 ATGGCCGTAG GGAAGTCCT GCTGGCTCT CTGCTGCTCC TGTCCCTGCA GCTGGGACAG
 TACCGGCATC CCTTCAAGGA CGACCCGAGA GACGACGAGG ACAGGGACGT CGACCCCTGTC
 1 M A V G K F L L G S L L L L S L Q L G Q
 61 GGCTGGGGCC CCGATGCCCG TGGGGTTCCC GTGGCCGATG GAGAGTTCTC GTCTGAACAG
 CCGACCCCGG GGCTACGGGC ACCCCAAGGG CACCGGCTAC CTCTCAAGAG CAGACTTGTC
 21 G W G P D A R G V P V A D G E F S S E Q
 **
 121 GTGGCAAAGG CTGGAGGGAC CTGGCTGGC ACCCACCGCC CCCTTGCCTCG CCTGCGCCGA
 CACCGTTCC GACCTCCCTG GACCGACCCG TGGGTGGCGG GGAACGGGC GGACGCGGCT
 41 V A K A G G T W L G T H R P L A R L R R
 181 GCCCTGTCTG GTCCATGCCA GCTGTGGAGC CTGACCCCTGT CCGTGGCAGA GCTAGGCCTG
 CGGGACAGAC CAGGTACGGT CGACACCTCG GACTGGGACA GGCACCGTCT CGATCCGGAC
 61 A L S G P C Q L W S L T L S V A E L G L
 *
 241 GGCTACGCCT CAGAGGAGAA GGTCACTTC CGCTACTGCG CCGGCAGCTG CCCCCGTGGT
 CCGATGCGGA GTCTCCTCTT CCAGTAGAAG GCGATGACGC GGCGTGCAC GGGGCACCA
 81 G Y A S E E K V I F R Y C A G S C P R G
 301 GCCCGCACCC AGCATGGCCT GCGCTGGCC CGGCTGCAGG GCCAGGGCCG AGCCCACGGT
 CGGCGTGGG TCGTACCGGA CCGCGACCCG GCCGACGTCC CGGTCCCGGC TCGGGTGCCA
 101 A R T Q H G L A L A R L Q G Q G R A H G
 361 GGGCCCTGCT GCCGGCCAC TCGCTACACC GACGTGGCCT TCCTCGATGA CCGCCACCGC
 CCCGGGACGA CGGCGGGGTG AGCGATGTGG CTGCACCGGA AGGAGCTACT GGCGGTGGCG
 121 G P C C R P T R Y T D V A F L D D R H R
 421 TGGCAGCGGC TGCCCCAGCT CTCGGCGGCT GCCTGCGGCT GTGGTGGCTG A
 ACCGTCGCCG ACGGGGTCGA GAGCCGCCGA CGGACGCCGA CACCACCGAC T
 141 W Q R L P Q L S A A A C G C G G

Figure 24